

amylase of *Streptomyces griseus* from the cytoplasm of said bacterium to a broth as the polypeptide encoded by SEQ ID NO:1 nucleotides 34 to 1944; and

b) an isolated polynucleotide encoding a polypeptide consisting of an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:4, wherein said polypeptide has at least the same activity in promoting excretion of an amylase of *Streptomyces griseus* from the cytoplasm of said bacterium to a broth as the polypeptide encoded by SEQ ID NO:2 nucleotides 22 to 1230.

21. (New) A *Corynebacterium glutamicum* bacterium comprising at least one isolated *Corynebacterium glutamicum* polynucleotide selected from the group consisting of:

a) an isolated polynucleotide encoding a polypeptide consisting essentially of the amino acid sequence of SEQ ID NO:3, wherein said polypeptide has at least the same activity in promoting excretion of an amylase of *Streptomyces griseus* from the cytoplasm of said bacterium to a broth as the polypeptide encoded by SEQ ID NO:1 nucleotides 34 to 1944; and

b) an isolated polynucleotide encoding a polypeptide consisting essentially of the amino acid sequence of SEQ ID NO:4, wherein said polypeptide has at least the same activity in promoting excretion of an amylase of *Streptomyces griseus* from the cytoplasm of said bacterium to a broth as the polypeptide encoded by SEQ ID NO:2 nucleotides 22 to 1230.

22. (New) Bacterium according to claim 21, wherein the polynucleotide of part a) comprises a sequence modification that results in (1) the substitution of one amino acid in the resulting polypeptide, (2) the deletion of one amino acid in the resulting polypeptide, or (3) the insertion of one amino acid in the resulting polypeptide, wherein said polypeptide has the

same activity in promoting excretion of an amylase of *Streptomyces griseus* from the cytoplasm of said bacterium to a broth as the polypeptide encoded by SEQ ID NO:1 nucleotides 34 to 1944.

23. (New) Bacterium according to claim 21, wherein the polynucleotide of part b) comprises a sequence modification that results in (1) the substitution of one amino acid in the resulting polypeptide, (2) the deletion of one amino acid in the resulting polypeptide, or (3) the insertion of one amino acid in the resulting polypeptide, wherein said polypeptide has the same activity in promoting excretion of an amylase of *Streptomyces griseus* from the cytoplasm of said bacterium to a broth as the polypeptide encoded by SEQ ID NO:2 nucleotides 22 to 1230.

24. (New) A *Corynebacterium glutamicum* bacterium comprising at least one isolated *Corynebacterium glutamicum* polynucleotide selected from the group consisting of:

a) an isolated polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:3; and


b) an isolated polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:4.

25. (New) Bacterium of claim 24, wherein said polypeptide comprising the amino acid sequence of SEQ ID NO:3 has at least the activity of promoting excretion of an amylase from the cytoplasm of said bacterium to a broth.

26. (New) Bacterium of claim 24, wherein said polypeptide comprising the amino acid sequence of SEQ ID NO:4 has at least the activity of promoting excretion of an amylase from the cytoplasm of said bacterium to a broth.

27. (New) A *Corynebacterium glutamicum* bacterium comprising at least one *Corynebacterium glutamicum* polynucleotide selected from the group consisting of:

- a) an isolated polynucleotide comprising SEQ ID NO:1 nucleotides 34 to 1944; and
- b) an isolated polynucleotide comprising SEQ ID NO:2 nucleotides 22 to 1230.

 28. (New) Bacterium of claim 27, wherein said isolated polynucleotide comprising SEQ ID NO:1 nucleotides 34 to 1944 encodes a polypeptide having at least the activity of promoting excretion of an amylase from the cytoplasm of said bacterium to a broth.

29. (New) Bacterium of claim 27, wherein said isolated polynucleotide comprising SEQ ID NO:2 nucleotides 22 to 1230 encodes a polypeptide having at least the activity of promoting excretion of an amylase from the cytoplasm of said bacterium to a broth.

30. (New) Bacterium of any of the claims 20, 21, 22, 23 and 24 comprising an isolated polynucleotide encoding a polypeptide, wherein said polypeptide is overexpressed.

31. (New) Bacterium of claims 28 or 29 comprising an isolated polynucleotide encoding a polypeptide, wherein said polypeptide is overexpressed.

32. (New) A vector comprising an isolated polynucleotide as set forth in any of claims 20, 21, 22, 23, 24 and 27.


33. (New) Bacterium of any of the claims 20, 21, 22, 23, 24 and 27, whereby in said bacterium at least one polypeptide selected from the group consisting of the secretory polypeptide *SecE* encoded by the *secE* gene native to *Corynebacterium glutamicum*, the secretory polypeptide *SecY* encoded by the *secY* gene native to *Corynebacterium glutamicum* and the secretory polypeptide *SecA* encoded by the *secA* gene native to *Corynebacterium glutamicum* is overexpressed.

34. (New) Bacterium of any of the claims 20, 21, 22, 23, 24 and 27, wherein said bacterium further comprises a nucleic acid encoding a heterologous polypeptide.

35. (New) Bacterium of claim 34, wherein said nucleic acid encoding a heterologous polypeptide is selected from the group consisting of a nucleic acid encoding a cellulase, a nucleic acid encoding an interferon, a nucleic acid encoding a lipase, and a nucleic acid encoding a nuclease.

36. (New) Bacterium of claim 34, wherein said nucleic acid encoding a heterologous polypeptide is a nucleic acid encoding a cellulase.

37. (New) Bacterium of claim 34, wherein said nucleic acid encoding a heterologous polypeptide is a nucleic acid encoding an amylase.

 38. (New) Bacterium of claim 37, wherein said nucleic acid encoding an amylase is a nucleic acid to the genus Streptomyces.

39. (New) Bacterium of claim 38, wherein said nucleic acid of the genus Streptomyces is native to the species Streptomyces griseus.

II. REMARKS

Support for new claims 20-39 is found throughout the application as originally filed. No new matter is believed to have been introduced herein.

Claims 1-8 were rejected under 35 U.S.C. § 112, first paragraph, as allegedly containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention.

The claimed invention allegedly encompasses any genetically modified Corynebacterium glutamicum strain having any genetic modification of the secD gene, secF gene, or "respective homologous sequences;" any genetically modified Corynebacterium glutamicum strain having any mutation, deletion, insertion, or rearrangement to the secD gene, secF gene, or their respective promoters; any genetically modified Corynebacterium glutamicum strain having any genetic modification of the secD gene, secF gene, or "respective homologous sequences" and further containing any heterologous gene which enables the strain to use any external energy source not used by the wild type Corynebacterium glutamicum or enables the strain to produce any substance which is a